

1/24

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1/24

2/24	3/24
4/24	5/24
6/24	7/24

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- 60	tgaaaagatagaataaatggcctcgtg
1	<u>ATGGCGCGGCCAGCGCTGCTGGGCGAG</u>
1	M A R P A L L G E
61	<u>GGCCAAGTTGCCCGCGGCCACAGAAGTT</u>
211	G Q V A A A T E V
121	GAAAATCTCTGCACGATAATATGGACG
41	E N L C T I I W T
181	ACTCTCAGATATTTTAGTCACTTTGAT
61	T L R Y F S H F D
241	CATCGTAAAGAGGAATTACCCCTGGAT
81	H R K E E L P L D
301	AGTGCCAATGAAAGTGAGAAGCCTAGC
101	S A N E S E K P S
361	GCTGATCCTGAGTCCGCTGTGACTGAG
121	G D P E S A V T E
421	AAGTGTTCCTGGCTCCCTGGAAGGAAT

Fig. 1(i)

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ccgaattcggcaccgagccgagggcgagggcctgc

CTGTTGGTGCTGCTACTGTGGACCGCCACCGTG

L L V L L L W T A T V

CAGCCACCTGTGACGAATTTGAGCGTCTCTGTG

Q, P P V T H L S V S V

TGGAGTCCTCCTGAACGAGCCAGTCCAAATTGC

W S P P E G A S P N C

GACCAACAGGATAAGAAAAATTGCTCCAGAAACT

D Q Q D K K I A P E T

GAGAAAATCTGTCTGCAGGTGGGCTCTCAGTGT

E K I C L Q V G S Q C

CCTTTGGTGAAAAAGTGCATCTCACCCCCCTGAA

P L V K K C I S P P E

CTCAAGTGCATTTGGCATAACCTGAGCTATATG

L K C I W H N L S Y M

ACAAGCCCTGACACACACTATACTCTGTACTAT

Fig. 1(ii)

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[illegible]

Fig. 1 (iii)

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CAATGTGAAAACATCTATAGAGAAGGTCAACAC
Q C E N I Y R E G Q H

GTGGAACCTAGTTTTGAACATCAGAACGTTCAA
V E P S F E H Q N V Q

ATPAGGCCATCCTGCCAAAATAGTGTCTTTAACT
I R P S C K I V S L T

ATTAAACATCTTCTCCTCAAAAATGGTGCCTTA
I K H L L L K N G A L

TTTAGAAGCAGATGCTTAACTTATGAAGTGGAG
F R S R C L T Y E V E

AATATTTTAGAGGTTGAAGAGGACAAATGCCAG
N I L E V E E D K C Q

GGTACAAAGTTGTTTCCAACTCCTGCTGTTCTT
G T S C F Q L P G V L

AGAGTCAAAACAAACAAGTTATGCTTTGATGAC
R V K T N K L C F D D

Fig. 1(iv)

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1021 TTCTACACCACCAATGTTACTCACCATT
341 F Y T T M L L T I

1081 CTTTCTACCTGAAAAGGCTTAAGATC
361 L F Y L K R L K I

1141 ATTTTAAAGAAATGTTTGGAGACCAG
381 I F K E M F G D Q

1201 ATCTATGAGAAACAATCCAAAGAAGAA
401 I Y E K Q S K E E

1261 AAAGCAGCTCCTTGATgggggagaagtg
421 K A A P *

1321 gatttattgcattctccatttggtatc

1381 ctggaaaaacaggcagctcctaagagc

1441 ccaaacccaaaggagctccttccaaga

1501 ccctaaaagcagatgttttgccaaatc

1561 accatcaattcattctaatacaggaattg

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CCAGTCTTTGTCCGAGTGGCAGTCATAATCCTC
P V F V A V A V I I L

ATTATATTTCTCCAATTCCTGATCCTGGCAAG¹
P I F P P I P D P G K

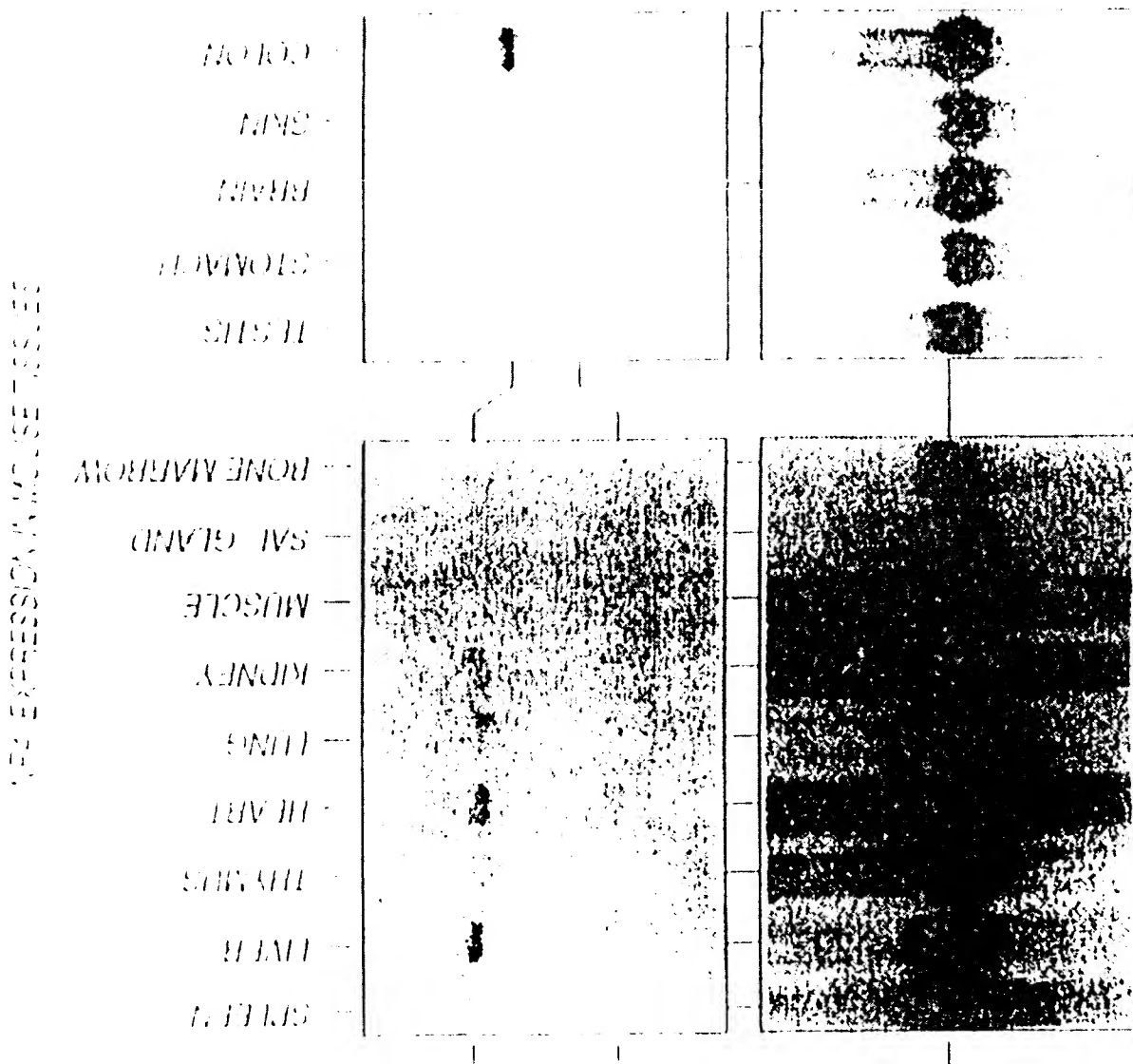
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ACCGATTCTCTAGTGCTCATAGAAAACCTGAAG
T D S V V L I E N L K

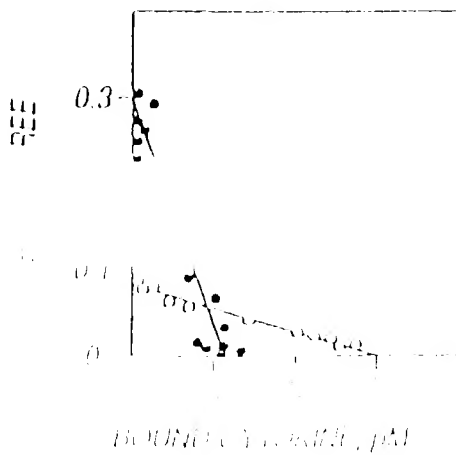
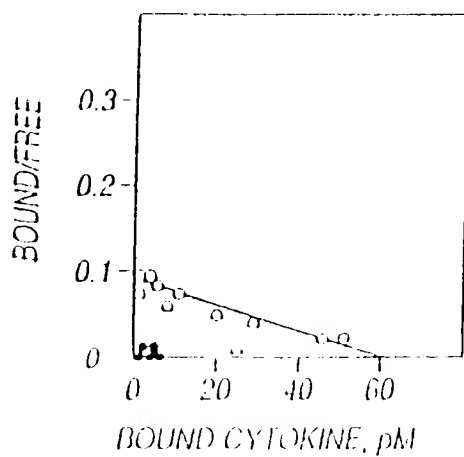
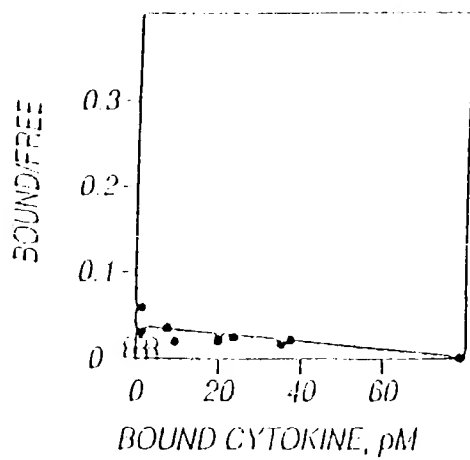
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tgatggcttcttaaggaatctctgcttgctctg

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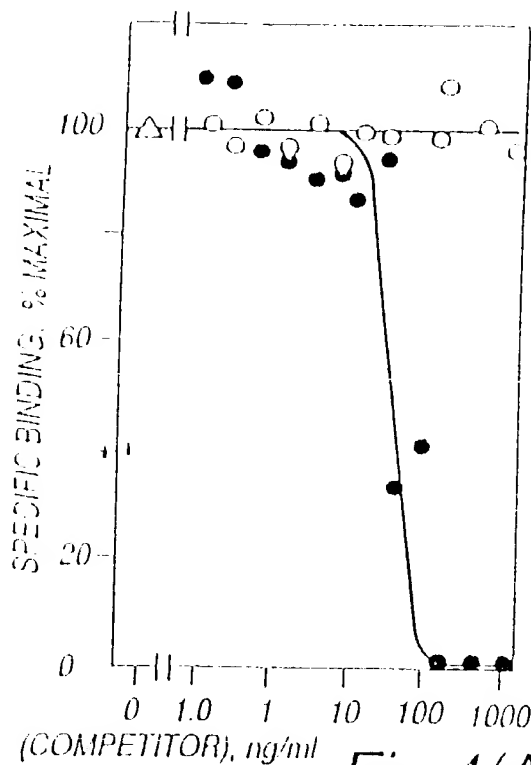


Fig. 4(A)

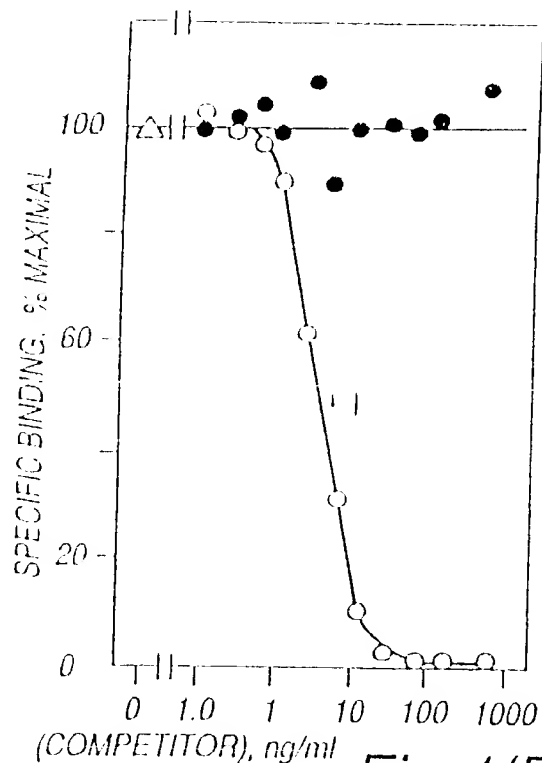
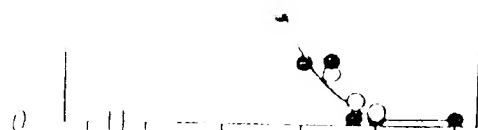
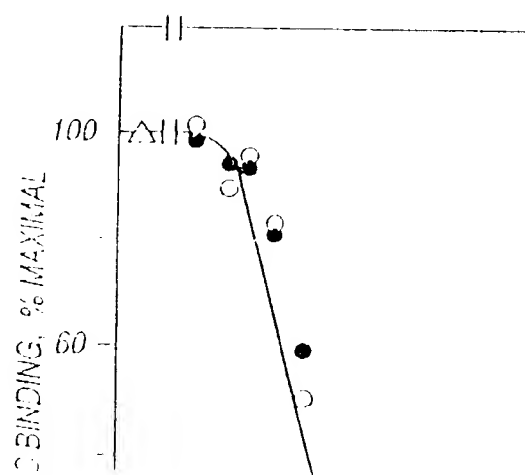
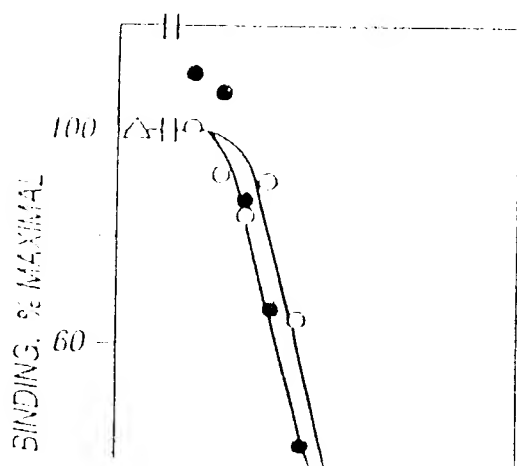


Fig. 4(B)



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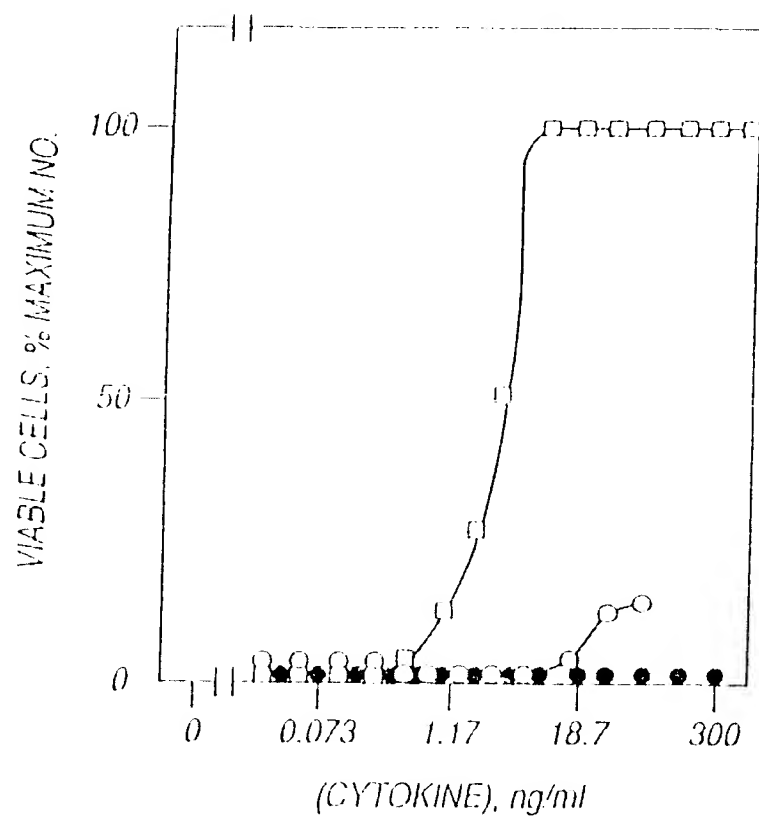
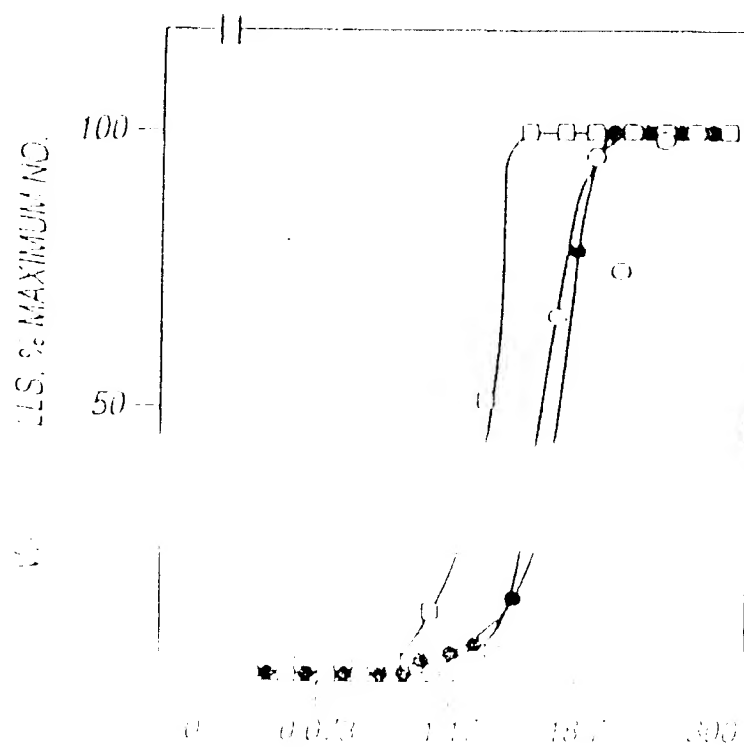


Fig. 5(A)



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CROSS SPECIES COMPARISON OF THE *hprt* GENE

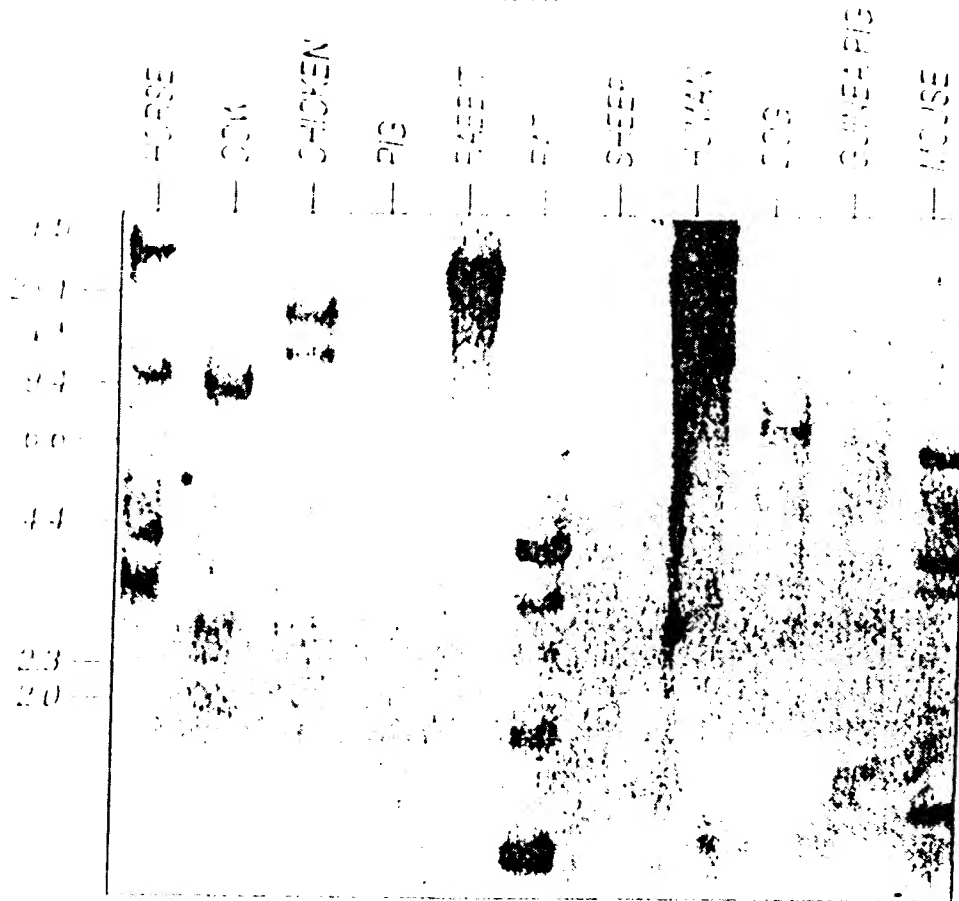


Fig. 6

(continued)

(continued)

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18/24	19/24
20/24	21/24

Fig. 7

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H		gagtcctaacacggaccaaggagttttaac
M	- 60	tgaaaagatagaataaatggcctcgtgc
H		M E W P A R L C G
		ATGGAGTGGCCCGCGCGCCTCTGCGGGC
		* * * *
M	11	ATGCGCGCGGCCAGCGCTCCTGGGCGAGC
M	1	M A R P A L L G E
H		G G G G A P T E T
H		GGGGGCGGGGGCGCGCCTACGGAAACTC
		* * * *
M	61	GGCCAAGTTGCCCGCGGCCACAGAAGTTC
M	21	G Q V A A A T E V
H		E N L C T V I W T
H		GAAAACCTCTGCACAGTAATATGGACAT
		* * * * *
M	121	GAAAATCTCTGCACGATAATATGGACGT
M	41	E N L C T I I W T
H		S L W Y F S H F G
H		AGTCTATGCTATTTTAGTCATTTTGGCG
		* * * * *
M	181	ACTCTCAGATATTTTAGTCACTTTGATC

Fig. 7(i)

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acgtgcggccgggttccgagggcgagaggetgc

.....
cgaattcggcaegagccgagggcgagggcctgc

L W A L L I C A G G G G
TGTGGGCGCTGCTGCTCTGCGCCGGCGGCGGGGGC.
* * * * *

TTTGGTGCTGCTACTCTGGACCGCCACCGTC - - -
L L V L L L W T A T V -

Q P P V T N L S V S V
AGCCACCTGTGACAAATTTGAGTGTCTCTGTT
* * * * *
AGCCACCTGTGACGAATTTGAGCGTCTCTGTC
Q P P V T N L S V S V

W N P P E G A S S N C
GGAATCCACCCGAGGGAGCCACCTCAAATTGT
* * * * *
GGACTCCTCCTGAAGGAGCCAGTCCAAATTGC
W S P P E G A S P N C

D K Q D K K I A P E T
ACAAACAAGATAAGAAAAATAGCTCCGGAAACT
* * * * *
ACCAACAGGATAAGAAAAATAGCTCCAGAAACT

Fig. 7(ii)

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H		R R S I E V P L N
H		CGTCCTTCAATAGAACTACCCCTGAATC * * * *
M	241	CATCGTAAAGAGGAATTACCCCTGGATC
M	81	H R K E E L P L D
H		S T N E S E K P S
H		AGCACCAATGAGAGTGAGAAGCCTAGCA * * * * * * * *
M	301	AGTGCCAATGAAAGTGAGAAGCCTAGCC
M	101	S A N E S E K P S
H		G D P E S A V T E
H		GGTGATCCTGACTCTGCTGTGACTGAAC * * * * * * * * *
M	361	GGTGATCCTGAGTCCGCTGTGACTGAGC
M	121	G D P E S A V T E
H		K C S W L P G R N
H		AAGTGTTCTTGGCTCCCTGGAAGGAATA * * * * * * * * *
M	421	AAGTGTTCTTGGCTCCCTGGAAGGAATA
M	141	K C S W L P G R N
H		W H R S L E K I H
H		AGGCAGTAATGAGAGTGAGAAGCCTAGCA * * * * * * * *

Fig. 7(iii)

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E	R	I	C	L	Q	V	G	S	Q	C
AGAGGATTTGTCTGCAAGTGGGGTCCCAGTGT										
*		*	*	*	*	*	*	*	*	*
A	G	A	A	A	T	C	T	C	T	G
CAGCTGGGCTCTCAGTGT										
E	K	I	C	L	Q	V	G	S	Q	C
11										
I	L	V	E	K	C	I	S	P	P	E
TTTGGTTGAAAAATGCATCTCACCCCCAGAA										
*	*	*	*	*	*	*	*	*	*	*
C	T	T	G	G	T	G	A	A	A	A
AGTGCATCTCACCCCCCTGAA										
P	L	V	K	K	C	I	S	P	P	E
L	Q	C	I	W	H	N	L	S	Y	M
TTCAATGCATTTGGCACAACTGAGCTACATG										
*	*	*	*	*	*	*	*	*	*	*
T	C	A	A	G	T	G	C	A	T	T
TGGCATAACCTGAGCTATATG										
L	K	C	I	W	H	N	L	S	Y	M
T	S	P	D	T	H	Y	T	L	Y	Y
CCAGTCCCCGACACTAACTATACTCTCTACTAT										
*	*	*	*	*	*	*	*	*	*	*
C	A	A	G	C	C	C	T	G	A	C
ACACACTATACTCTGTACTAT										
T	S	P	D	T	H	Y	T	L	Y	Y
T P D T P P E C O Y										

Fig. 7(iv)

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			*		*	*	*	*	
M	481	TGGTACAGCAGCCTGGAGAAAAGTCGTC							
M	161	W Y S S L E K S R							
H		F G C S F D L T K							
H		TTTGCTTGCTTCCTTTGATCTGACCAAAG							
			*	*	*		*	*	*
M	541	ATTGCTTGCTTCCTTTAAATTGACTAAAG							
M	181	I A C S F K L T K							
H		Q I M V K D N A G							
H		CAAATAATGCTCAAGGATAATGCAGGAA							
			*	*	*	*	*	*	*
M	601	CAAATAATGGTCAAGGATAATGCTGGGA							
M	201	Q I M V K D N A G							
H		T S R V K P D P P							
H		ACTTCCCCGTGTGAAACCTGATCCTCCAC							
			*	*	*	*	*	*	*
M	661	ACTTCCTATGTGAAACCTGATCCTCCAC							
M	221	T S Y V K P D P P							
H		L Y V Q W E N P Q							
H		CTATATGTGCAATGGGAGAATCCACAGA							
			*	*	*	*	*	*	*
M	721	TTATTACTCCAGTGGGAAGAATCCACAAA							

Fig. 7(v)

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```
* * * * * * * *
AATGTGAAAACATCTATAGAGAAGGTCAACAC
Q C E N I Y R E G Q H

V K D S S F E Q H S V
TGAACGATTCCAGTTTGAACAACACAGTGTC
* * * * *
TGGAACCT- - - AGTTTTC AACATCAGAACG TT
V E P - S F E H Q N V

K I K P S F N I V P L
AAATTAAACCATCCTTCAATATAGTGCCTTTA
* * * * *
AAATTAGGCCATCCTGC AAAATAGTGTCTTTA
K I R P S C K I V S L

H I K N L S F H N D D
ATATTAAAAACCTCTCCTTCACAATGATGAC
* * * * *
ATATTAAACATCTTCTCCTCAAAAATGGTGCC
H I K H L L L K N G A

H F I S R C L F Y E V
ATTTTATTAGCAGATGCCTATTTTATGAAGTA
* * * * *
ATTTTAGAAGCAGATGCTTAAC TTATGAAGTG
```

Fig. 7(vi)

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H		E	V	N	N	S	Q	T	E	T
H		GAAGTCAATAACAGCCAAACTGAGACAC								
		*	*	*	*		*	*		
M	781	GAGGTCAATAATACTCAAACCGACCGAC								
M	261	E	V	N	N	T	Q	T	D	R
H		E	N	P	E	F	E	R	N	V
H		GAGAATCCAGAATTTGAGAGAAATGTGG								
		*		*			*	*		
M	841	CAGAATTCCGAATCTGATAGAAACATCG								
M	281	Q	N	S	E	S	D	R	N	M
H		L	P	D	T	L	N	T	V	R
H		CTTCCTGATACTTTGAACACAGTCAGAA								
		*		*			*	*	*	
M	901	CTTGCCCGACGCTGTCTACACAGTCAGAG								
M	301	L	A	D	A	V	Y	T	V	R
H		D	D	K	L	W	S	N	W	S
H		GATGACAAACTCTGGAGTAATTGGAGCC								
		*		*	*	*	*		*	*
M	961	GACAACAAACTCTGGAGTGATTGGAGTG								
M	321	D	N	K	L	W	S	D	W	S
H										

Fig. 7(vii)

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H N V F Y V Q E A K C
ATAATGTTTTCTACGTCCAAGAGGCTAAATGT
* * * * *
ATAATATTTTAPAGAGGTTGAAGAGGACAAATCC
H N I L E V E E D K C
E N T S C F M V P G V
AGAATACATCTTGTTCATGCTCCCTGGTGTT
* * * * *
AGGGTACAAGTTGTTTCCAACCTCCCTGGTGTT
E G T S C F Q L P G V
I R V K T N K L C Y E
TAAGAGTCAAAAACAAATAAGTTATGCTATGAG
* * * * *
TAAGAGTCAAAAACAAACAAGTTATGCTTTGAT
V R V K T N K L C F D
Q E M S I G K K R N S
AAGAAAATGAGTATAGCTAAGAAGCCGCAATTCC
* * * * *
AAGCACAGAGTATAGGTAAGGAGCAAAACTCC
E A Q S I G K E Q N S
V P V T V A G A I T V

Fig. 7(viii)

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			*	*		*	*	*	*
M	1021	ACCTTCTACACCACCATGTTACTCACCA							
M	341	T F Y T T M L L T							
H		L L L Y L K R L K							
H		CTCCTGCTTTACCTAAAAAGGCTCAAGA							
		* * * * *							
M	1081	CTCCTT TTTTACCTGAAAAGGCTTAAGA							
M	361	L L F Y L K R L K							
H		K I F K E M F G D							
H		AAGATTTTTTAAAGAAATGTTTGGAGACC							
		* * * * *							
M	1141	AAGATTTTTTAAAGAAATGTTTGGAGACC							
M	381	K I F K E M F G D							
H		D I Y E K Q T K E							
H		GACATCTATGAGAAGCAAACCAAGGAGG							
		* * * * *							
M	1201	GACATCTATGAGAACAATCCAAAGAAG							
M	401	D I Y E K Q S K E							
H		K K A S Q *							
H		AAGAAAGCCTCTCAGTGATggagataat							
		* * *							
M	1261	AAGAAAGCAGCTCCTTGATgggggagaag							
M	121	K K A S Q *							

Fig. 7(ix)

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```

      *   *       *   *       *       *
TTCCAGTCTTTGTGCGCAGTGGCAGTCATAATC
I   P   V   F   V   A   V   A   V   I   I

I   I   I   F   P   P   I   P   D   P   G
TTATTATATTCCCTCCAATTCCTGATCCTGGC
      *   *   *   *   *   *   *   *   *   *
TCATTATATTTCCCTCCAATTCCTGATCCTGGC
I   I   I   F   P   P   I   P   D   P   G

Q   N   D   D   T   L   H   W   K   K   Y
AGAATGATGATACTCTGCACTGGAAGAAGTAC
      *   *   *   *   *   *   *   *   *   *
AGAATGATGATACCCTGCACTGGAAGAAGTAT
Q   N   D   D   T   L   H   W   K   K   Y

E   T   D   S   V   V   L   I   E   N   L
AAACCGACTCTGTACTGCTGATAGAAAACCTG
      *   *   *   *   *   *   *   *   *   *
AAACCGATTCTGTACTGCTGATAGAAAACCTG
E   T   D   S   V   V   L   I   E   N   L

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tgattttctttctttgccttcaatgtgacctgt

```

Fig. 7(x)

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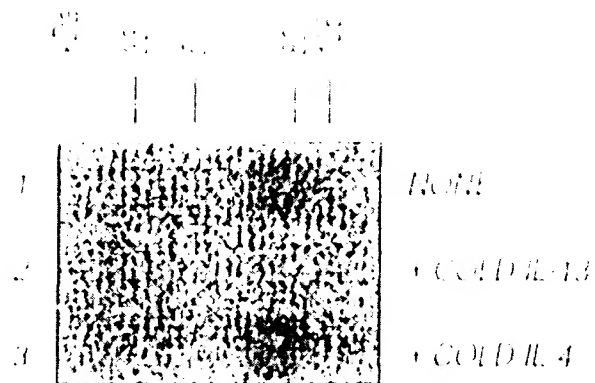


Fig. 8

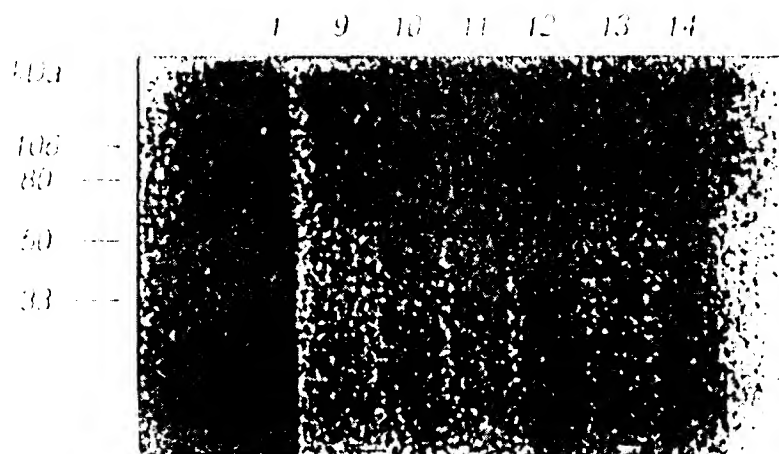


Fig. 9